

RESPONSE

Serial No. 09/954,695
Atty. Docket No. GP116-02.UTMarked-Up Version of AmendmentsIN THE CLAIMS:

The claims have been amended as follows:

9. (Amended) The probe of claim 8, wherein said probe comprises two of said one or more base sequences, wherein said two base sequences hybridize to each other when said probe is not hybridized to [said] the target sequence under the stringent conditions.

16. (Amended) A hybridization assay probe comprising an oligonucleotide which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, wherein [the base sequence of] said oligonucleotide has a base sequence which is at least 80% complementary to the base sequence of the target sequence, wherein the target sequence is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

19. (Amended) A probe mix comprising the probe of claim 1 and [one or more] a first helper [oligonucleotides] oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence, wherein the target sequence of said first helper oligonucleotide is selected from the group consisting of SEQ ID NO:21, [SEQ ID NO:22,] SEQ ID NO:23, [SEQ ID NO:24,] SEQ ID NO:25[, SEQ ID NO:26,] and SEQ ID NO:27 [and SEQ ID NO:28].

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21. (Amended) The probe mix of claim 19 further comprising a second helper oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence, wherein the target sequence of said second helper oligonucleotide [one of said helper oligonucleotides] is selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28.

23. (Amended) An amplification primer for use in amplifying a nucleic acid sequence present in nucleic acid derived from a *Cryptosporidium* organism under amplification conditions, said primer comprising an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group consisting of [SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47,] SEQ ID NO:48, [SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53,] SEQ ID NO:54, [SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59,] SEQ ID NO:60[, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65,] and SEQ ID NO:66, [SEQ ID NO:67 and SEQ ID NO:68,] wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

38. (Amended) An amplification primer for use in amplifying a nucleic acid sequence present in nucleic acid derived from a *Cryptosporidium* organism under amplification conditions, said primer comprising an oligonucleotide[, wherein the] having a base sequence [of said oligonucleotide] which is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of [SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47,] SEQ ID NO:48, [SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53,] SEQ ID NO:54, [SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59,] SEQ ID NO:60[, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65,] SEQ ID NO:66, [SEQ ID NO:67 and SEQ ID NO:68,] wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

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NO:65,] and SEQ ID NO:66, [SEQ ID NO:67 and SEQ ID NO:68,] and wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

39. (Amended) An amplification primer for use in amplifying a nucleic acid sequence present in nucleic acid derived from a *Cryptosporidium* organism under amplification conditions, wherein the base sequence of said primer is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of [SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47,] SEQ ID NO:48, [SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53,] SEQ ID NO:54, [SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59,] SEQ ID NO:60[, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65,] and SEQ ID NO:66, [SEQ ID NO:67 and SEQ ID NO:68,] and wherein said oligonucleotide optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

40. (Amended) An amplification primer for use in amplifying a nucleic acid sequence present in nucleic acid derived from a *Cryptosporidium* organism under amplification conditions, wherein the base sequence of said primer is fully complementary to the base sequence of a target sequence selected from the group consisting of [SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47,] SEQ ID NO:48, [SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53,] SEQ ID NO:54, [SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59,] SEQ ID NO:60[, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65,] and SEQ ID NO:66, [SEQ ID NO:67 and SEQ ID NO:68,] and wherein said oligonucleotide optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

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41. (Amended) A set of amplification primers for use in amplifying a nucleic acid sequence present in nucleic acid derived from a *Cryptosporidium* organism under amplification conditions, [wherein at least two primers of said set of primers comprise] said set of primers including first and second primers, wherein:

said first primer is said primer of claim 23; and

said second primer comprises an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, [SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50,] SEQ ID NO:51, SEQ ID NO:52, [SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56,] SEQ ID NO:57, SEQ ID NO:58, [SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62,] SEQ ID NO:63[,] and SEQ ID NO:64, [SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67 and SEQ ID NO:68,] wherein one or more primers of said set of primers optionally include a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

43. (Amended) The [method] primer set of claim 41, wherein[said set of primers includes:

a first primer, wherein] the target sequence of said [first] second primer is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63[; and

a second primer, wherein the target sequence of said second primer is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66].

45. (Amended) The [method] primer set of claim 41, wherein[said set of primers includes:

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a first primer, wherein] the target sequence of said [first] second primer is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64[; and

a second primer, wherein the target sequence of said second primer is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66].

74. (Amended) A kit comprising, in packaged combination, [two or more] first and second oligonucleotides for use in determining the presence of a *Cryptosporidium* organism in a test sample, each of said oligonucleotides having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium* organism, wherein;

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3[,] and SEQ ID NO:4;

the target sequence of said second oligonucleotide is selected from the group consisting of [, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47,] SEQ ID NO:48, [SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53,] SEQ ID NO:54, [SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59,] SEQ ID NO:60[,] and [SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65,] SEQ ID NO:66[, SEQ ID NO:67 and SEQ ID NO:68,]; and

[wherein one or more of] said [oligonucleotides] second oligonucleotide optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

83. (Amended) The [method] kit of claim 74 [82 wherein:] further comprising a third oligonucleotide, wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target

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sequence contained in nucleic acid derived from a *Cryptosporidium* organism, and wherein the target sequence of said [second] third oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63[; and

wherein the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65].

85. (Amended) The [method] kit of claim 74 [82, wherein:] further comprising a third oligonucleotide, wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium* organism, and wherein the target sequence of said [second] third oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64[; and

the target sequence of third oligonucleotide is selected from the group consisting of SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59 and SEQ ID NO:65].

88. (Amended) A kit comprising, in packaged combination, [said probe of claim 1 and at least one helper oligonucleotide] first and second oligonucleotides for use in determining the presence of a *Cryptosporidium* organism in a test sample, each of said oligonucleotides having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium* organism, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:21, [SEQ ID NO:22,] SEQ ID NO:23, [SEQ ID NO:24,] SEQ ID NO:25[, SEQ ID NO:26,] and SEQ ID NO:27 [and SEQ ID NO:28].